

**WHAT IS CLAIMED IS:**

1           1.       A method for detecting dengue virus comprising:  
 2           obtaining a sample which is suspected of containing dengue virus RNA;  
 3           performing a reverse transcriptase-polymerase chain reaction on the sample with a first  
 4           dengue virus-specific primer and a second dengue virus-specific primer to amplify the dengue  
 5           virus RNA, if present, wherein the first dengue virus-specific primer is 18 to 28 nucleotides in  
 6           length and includes at least 18 consecutive nucleotides of SEQ ID NO:1, and the second dengue  
 7           virus-specific primer is 18 to 28 nucleotides in length and includes at least 18 consecutive  
 8           nucleosides of SEQ ID NO:2; and  
 9           detecting the amplification product as an indication of presence of dengue virus in the  
 10          sample.

1           2.       The method of claim 1, wherein the first dengue virus-specific primer is 18 to 23  
 2           nucleotides in length.

1           3.       The method of claim 1, wherein the first dengue virus-specific primer is the  
 2           nucleotide sequence of SEQ ID NO:1.

1           4.       The method of claim 1, wherein the second dengue virus-specific primer is 18 to  
 2           23 nucleotides in length.

1           5.       The method of claim 1, wherein the second dengue virus-specific primer is the  
 2           nucleotide sequence of SEQ ID NO:2.

1           6.       The method of claim 2, wherein the second dengue virus-specific primer is 18 to  
 2           23 nucleotides in length.

1           7.       The method of claim 3, wherein the second dengue virus-specific primer is the  
 2           nucleotide sequence of SEQ ID NO:2

1           8.       A method for quantitating dengue virus comprising:  
2           obtaining a sample which is suspected of containing dengue virus RNA, and mixing it  
3           with a known amount of a competitor nucleic acid;  
4           performing a reverse transcriptase-polymerase chain reaction on the sample and the  
5           competitor nucleic acid with a first dengue virus-specific primer and a second dengue virus-  
6           specific primer to amplify the dengue virus RNA, if present, and the competitor nucleic acid,  
7           wherein the first dengue virus-specific primer is 18 to 28 nucleotides in length and includes at  
8           least 18 nucleotides of SEQ ID NO:1, and the second dengue virus-specific primer is 18 to 28  
9           nucleotides in length and includes at least 18 nucleosides of SEQ ID NO:2; and  
10          comparing the amounts of the amplification product of the dengue virus RNA, if  
11          present, to the amplification product of the competitor nucleic acid to quantitate the dengue  
12          virus RNA in the sample.

1           9.       The method of claim 8, wherein the first dengue virus-specific primer is 18 to 23  
2           nucleotides in length.

1           10.      The method of claim 8, wherein the first dengue virus-specific primer is the  
2           nucleotide sequence of SEQ ID NO:1.

1           11.      The method of claim 8, wherein the second dengue virus-specific primer is 18 to  
2           23 nucleotides in length.

1           12.      The method of claim 8, wherein the second dengue virus-specific primer is the  
2           nucleotide sequence of SEQ ID NO:2.

1           13.      The method of claim 9, wherein the second dengue virus-specific primer is 18 to  
2           23 nucleotides in length.

1           14.      The method of claim 10, wherein the second dengue virus-specific primer is the  
2           nucleotide sequence of SEQ ID NO:2.

1 15. A kit for detecting dengue virus comprising:

2 A first dengue virus-specific primer, which is 18 to 28 nucleotides in length and includes  
3 at least 18 nucleotides of SEQ ID NO:1; and

4 A second dengue virus-specific primer, which is 18 to 28 nucleotides in length and  
5 includes at least 18 nucleotides of SEQ ID NO:2.

1 16. The kit of claim 15, further comprising a known amount of a competitor nucleic  
2 acid with length detectably different from the dengue virus RNA.

1 17. The kit of claim 15, wherein the first dengue virus-specific primer is 18 to 23  
2 nucleotides in length.

1 18. The kit of claim 15, wherein the first dengue virus-specific primer is the  
2 nucleotide sequence of SEQ ID NO:1.

1 19. The kit of claim 15, wherein the second dengue virus-specific primer is 18 to 23  
2 nucleotides in length.

1 20. The kit of claim 15, wherein the second dengue virus-specific primer is the  
2 nucleotide sequence of SEQ ID NO:2.

1 21. The kit of claim 17, wherein the second dengue virus-specific primer is 18 to 23  
2 nucleotides in length.

1 22. The kit of claim 18, wherein the second dengue virus-specific primer is the  
2 nucleotide sequence of SEQ ID NO:2.

1 23. A nucleic acid, which is 18 to 28 nucleotides in length and includes at least 18  
2 consecutive nucleotides of SEQ ID NO:1.

1 24. The nucleic acid of claim 23, wherein the nucleic acid is 18 to 23 nucleotides in  
2 length and includes at least 18 consecutive nucleotides of SEQ ID NO:1.

1           25.    The nucleic acid of claim 23, wherein the nucleic acid is the nucleotide sequence  
2 of SEQ ID NO:1.

1           26.    A nucleic acid, which is 18 to 28 nucleotides in length and includes at least 18  
2 consecutive nucleotides of SEQ ID NO:2.

1           27.    The nucleic acid of claim 26, wherein the nucleic acid is 18 to 23 nucleotides in  
2 length and includes at least 18 consecutive nucleotides of SEQ ID NO:2.

1           28.    The nucleic acid of claim 26, wherein the nucleic acid is the nucleotide sequence  
2 of SEQ ID NO:2.

1           29.    An isolated nucleic acid comprising a fragment of a dengue viral genome or a  
2 DNA copy thereof, wherein the fragment includes:  
3           a first sequence that is complementary or identical to at least 18 consecutive nucleotides  
4 of SEQ ID NO:1;  
5           a second sequence that is complementary or identical to at least 18 consecutive  
6 nucleotides of SEQ ID NO:2; and  
7           a non-naturally occurring deletion or insertion, the deletion or insertion occurring in a  
8 region of the fragment flanked by the first and the second sequence.

1           30.    The nucleic acid of claim 29, wherein the first sequence is complementary or  
2 identical to SEQ ID NO:1 and the second sequence that is complementary or identical to SEQ  
3 ID NO:2.